

# Model for Camel IgG 3

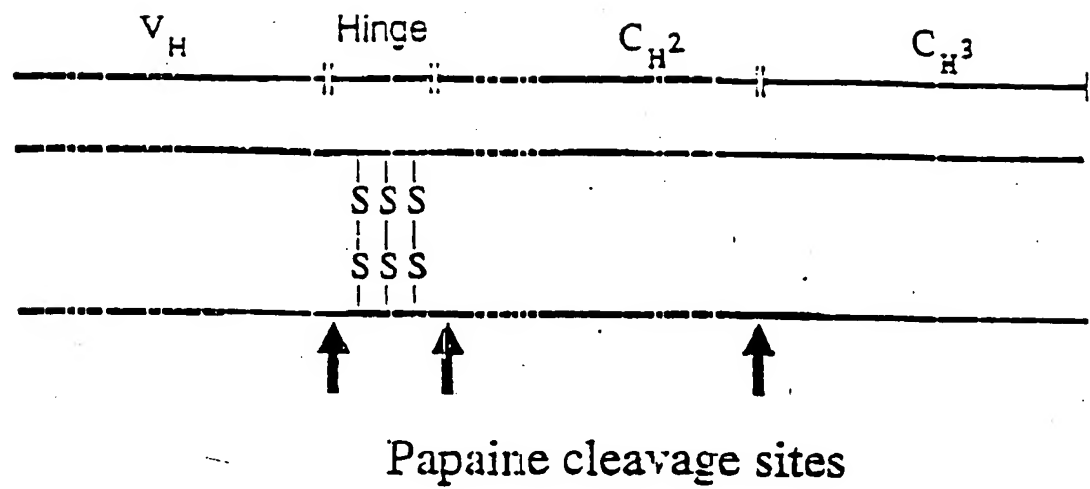


Fig 5: Schematic representation of Camel IgG<sub>3</sub> model.

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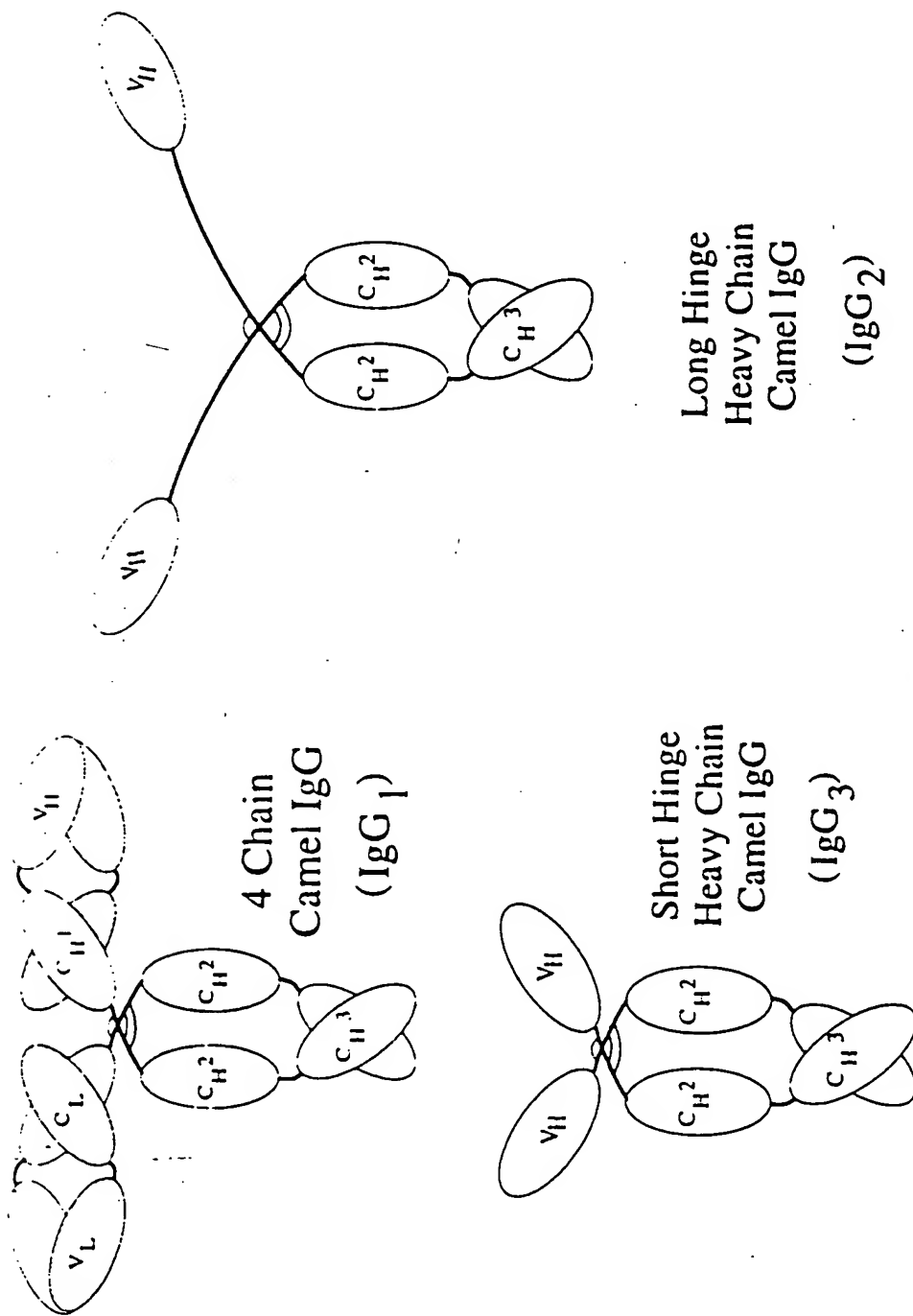


Fig 6 : A schematic representation of Camel immunoglobulins IgG<sub>1</sub>, the putative IgG<sub>2</sub> and IgG<sub>3</sub>. The large (Pro-X)<sub>12</sub> of the putative IgG<sub>2</sub> molecule can be modelled into a 6 aa repeat

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DR01006 C-----TCGAG---TCTGGGGGAGG
DR27006 C-----TCGAG---TCTGGGGGAGG
DR03006 C-----AGGTGA-----AACTGCTCGAG---TCTGGAGGAGG
DR11006 C-----TCGAG---TCTGGGGGAGG
DR24006 C-----AGGTGA-----AACTGCTCGAG---TCTGGGGGAGG
DR16006 C-----TCGAG---TCTGGAGGAGG
DR19006 C-----TCGAG---TCTGGAGGAGG
DR07006 C-----TCGAG---TCTGGGGGAGG
DR16006 C-----TCGAG---TCTGGGGGAGG
DR20006 C-----TCGAG---TCAGGGGGAGG
DR25006 C-----TCGAG---TCTGGGGGAGG
DR20006 C-----TCGAG---TCTGGAGGAGG
DR21006 C-----TCGAG---TCTGGGGGAGG
DR09006 C-----AGGTGA-----AACTGCTCGAG---TCTGGGGGAGG
DR17006 C-----TCGAG---TCTGGGGGAGG
DR13006 C-----TCGAG---TCAGGGGGAGG
DR02006 CTCGAGTCAGGTGTCCGGTCTGATGTGCAGCTGGTGGCGTCTGGGGGAGG

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DR11006 ATCGGTGCAGGCTGGAGGGTCTCTGAGACTCTC--GTGCG-CAGCCTCTG
DR07006 CTCGGTGCAGGCTGGAGGGTCTCTGAGACTCTCCTGTGCATCTTCTTCTA
DR13006 CTCGGTGCAGACTGGAGGATCTCTGAGACTCTCCTGTGCAGT--C-TCTG
DR11006 GTCGGTGCAGGCTGGAGGGTCTCTGAGACTCTCCTGTAATGT--C-TCTG
DR04006 GTCGGTGCAGGCTGGAGGGTCTCTGAGACTCTCCTGTAATGT--C-TCTG
DR16006 CTCGGCGCAGGCTGGAGGATCTCTGAGACTCTCCTGTGCAGC--CCACGG
DR19006 CTCGGTTCAGGCTGGAGGGTCCCTTAGACTCTCCTGTGCAGC--C-TCTG
DR17006 CTCGGTGCAGGGTGGAGGGTCTCTGAGACTCTCCTGTGCAA---TCTCTG
DR16006 CTCGGTGCAGGCTGGAGGGTCTCTGAGACTCTCCTGTACAG---GCTCTG
DR20006 CTCGGTACAGGTTGGAGGGTCTCTGAGACTCTCCTGTGTAG---CCTCTA
DR25006 CTCGGTACAACTGGAGGGTCTCTGAGACTCTCTTGCG---AAATCTCTG
DR08006 CTCGGTGCAGGCTGGAGGGTCTCTGAGACTCTCCTGTG---TAGCCTCTG
DR11006 CTCGGTGCAGGTTGGAGGGTCTCTGAAACTCTCCTGTAAAT---CTCTG
DR09006 CTCGGTGCAGGCTGGGGGGTCTCTGACACTCTCTTGTTG---TATACAC--
DR17006 CTCGGTCCAACCTGGAGGATCTCTGACACTCTCCTGTACAGTT---TCTG
DR13006 CTCGGTGGAGGCTGGAGGGTCTCTGAGACTCTCCTGTACAG---CCTCTG
DR02006 CTCGGTGCAGGCTGGAGGCTCTCTGAGACTCTCCTGTACAG---CCTCTG

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DR01006 GA--TACAGTAATT---GTCCCCTCACTTG-GAGCTGGTATCGCCAGTTT
DR27006 AA--TATATGCCTT---GCACCTACGACAT-GACCTGGTACCGCCAGGCT
DR03006 GA--TTCTCCTTTA---GTACCAGTTGTAT-GGCCTGGTTCCGCCAGGCT
DR11006 GC--TCTCCCAGTA---GTACTTATTGCCT-GGGCTGGTTCCGCCAGGCT
DR24006 GC--TCTCCCAGTA---GTACTTATTGCCT-GGGCTGGTTCCGCCAGGCT
DR16006 GA--TTCCGC-TCA---ATGGTTACTACAT-CGCCTGGTTCCGTCAGGCT
DR19006 AC--TACACCATCA---CTGATTATTGCAT-GGCCTGGTTCCGCCAGGCT
DR07006 GA--TACACGTACG---GTAGCTTCTGTAT-GGGCTGGTTCCGCCAGGGT
DR16006 GA--TTCCCCTATA---GTACCTTCTGTCT-GGGGTGGTTCCGCCAGGCT
DR20006 CT--CACACCGACA---GTAGCACCTGTAT-AGGCTGGTTCCGCCAGGCT
DR25006 GA--TTGACTTTTG---ATGATTCTGACGT-GGGGTGGTACCGCCAGGCT
DR20006 GA--TTCAATTTTCG---AACTTCTCGTAT-GGCGTGGTACCGCCAGACT
DR21006 GAGGTACCCCAGATCGTGTTCCTAAATCTTTGGCCTGGTTCCGCCAGGCT

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DR09006 -----CAACGATACTGGGACCA-----TGGGATGGTTTCCGCCAAGCT  
 DR17006 --GGGCCACCTACA---GTGACTACAGTATTGGA-TGGATCGGCCAAGCT  
 DR13006 G-----ATAGGTAT-CCT----CTATGGCCTGGTTCCGCCAAGCT  
 DR02006 GAGA----CAGTTTCAGTAGATT--TGCCATGTCTTGGTTCCGCCAAGCT

DR01006 CCAGGAACGGAGCGCGAGTTTCGTCTCCAGTATGGATCCGGATGGAAATAC  
 DR27006 CCAGGCAAGGAGCGCGAATTTGTCTCAAGTATAAATATTGATGGTAAGAC  
 DR03006 TCAGGAAAGCAGCGTGAGGGGGTTCGACAGCCATTAATAGTGGCGGTGGTAG  
 DR11006 CCAGGGAGGGAGCGTGAGGGGGTTCACAGCGATTAA-----CACTGATGG  
 DR24006 CCAGGGAAGGAGCGTGAGGGGGTTCACAGCGATTAA-----CACTGATGG  
 DR16006 CCTGGGAAGGGGCGTGAGGGGGTTCGCAACAATTAATGGTGGTTCG-----  
 DR19006 CCAGGGAAGGAGCGTGAATTGGTTCGACAGCGATTCAAGTTGTCCGTAGTGA  
 DR07006 CCAGGCAAGGAACGTGAGGGGATCGCAACTATTCTTAATGGTGGTACTAA  
 DR16006 CCAGGGAAGGAGCGTGAGGGGGTTCGCGGGTATTAATAGTGCAGGAGGTAA  
 DR20006 CCAGGGAAGGAGCGCGAGGGGGTTCGCAAGTATATATTTTGGTGTATGGTGG  
 DR25006 CCAGGGCATGAGTGCAAAATTGGTCTCAGGTATTCAGTGTATGGTACT-C  
 DR20006 CCAGGAAATGTGTGTGAGTTGGTCTCAAGTATTTACAGTGTATGG-----  
 DR21006 CCAGAGAAGGAGCGCGAGGGGATCGCAGTTCTTTTCGACTAAGGATGGTAA  
 DR09006 CCAGGGAAGAGTGCGAAAGGGTTCGCGCATATTACGCCTGATGGTATGA-  
 DR17006 CCAGGGAAGGACCGTGAAGTAGTTCGACGCCGCTAATACTGGTG-----  
 DR13006 CCAGGGCAGGAGCGCGAGGGGGTTCGCGTTTGTTCAAACGG-----  
 DR02006 CCAGGGAAGGAGTGCGAATTGGTCTCAAGCATTCAAAGTAATGGAAGGAC

DR01006 CAAGTACA-----CATACTCCGTGAAGGGCCGCTTCACC  
 DR27006 AACATACG-----CAGACTCCGTGAAGGGCCGATTTCACC  
 DR03006 GACATACTA-CAACACATATGTCGCCGAGTCCGTGAAGGGCCGATTTCGCC  
 DR11006 CAGTATCAT-ATACGCA-----GCCGACTCCGTGAAGGGCCGATTTCACC  
 DR24006 CAGTGTCTAT-ATACGCA-----GCCGACTCCGTGAAGGGCCGATTTCACC  
 DR16006 -----CGA-CGTACATACTACGCCGACTCCGTGACGGGCCGATTTACC  
 DR19006 TACT--CGC-C-TCACAGACTACGCCGACTCCGTGAAGGGACGATTTCACC  
 DR07006 -----CACATACTATGCCGACTCCGTGAAGGGCCGATTTCACC  
 DR16006 -----TACTTACTATGCCGACGCCGTGAAGGGCCGATTTCACC  
 DR20006 -----TACGAATTATCGCGACTCCGTGAAGGGCCGATTTCACC  
 DR25006 CATATACAAAGAGTGGAGACTATGCTGAGTCTGTGAGGGGCCGGTTACC  
 DR20006 CA-AAACATACTACGTCGACC--GCA-----TGAAGGGCCGATTTCACC  
 DR21006 GA-----CATTCTATGCCGACTCCGTGAAGGGCCGATTTCACC  
 DR09006 -----CCTTCATTGATGAACCCGTGAAGGGGCCGATTTCAG  
 DR17006 -----CGACTAGTAAATTCTACGTCGACTTTGTGAAGGGCCGATTTCACC  
 DR13006 --CTGACAAT-AGTGCATTATATGGCGACTCCGTGAAGGGCCGATTTCACC  
 DR02006 AACTGA-----GGCCGATTCCGTGCAAGGGCCGATTTCACC

DR01006 ATGTCCCGAGGCAGCACCGAGTACACAGTATTTCTGCAAATGGACAATCT  
 DR27006 ATCTCCCAAGACAGCGCCAAGAACACGGTGTATCTGCAGATGAACAGCCT  
 DR03006 ATCTCCCAAGACACCGCCAAGACCACGGTATATCTTGATATGAACAACCT  
 DR11006 ATCTCCCAAGACACCGCCAAGGAAACGGTACATCTCCAGATGAACAACCT  
 DR24006 ATCTCCCAAGACACCGCCAAGAAAACGGTATATCTCCAGATGAACAACCT  
 DR16006 ATCTCCCGAGACAGCCCCAAGAATACGGTGTATCTGCAGATGAACAGCCT  
 DR19006 ATCTCCCAAGGCAACACCAAGAACACAGTGAATCTGCAAATGAACAGCCT  
 DR07006 ATCTCCCAAGACAGCACGTTGAAGACGATGTATCTGCTAATGAACAACCT  
 DR16006 ATCTCCCAAGGGAATGCCAAGAATACGGTGTCTTCTGCAAATGGATAACTT  
 DR20006 ATCTCCCAACTCAACGCCCAGAACACAGTGTATCTGCAAATGAACAGCCT  
 DR25006 ATCTCCAGAGACAACGCCAAGAATACATTGTATCTACAACCTGAGCGGCCT  
 DR20006 ATTTCTAGAGAGAATGCCAAGAATACATTGTATCTACAACCTGAGCGGCCT  
 DR21006 ATCTTCTTAGATAATGACAAGACCCTTTCTCCTTACAACCTGATCGACT  
 DR09006 ATCTCCCGAGACAACGCCCAAGAAACGTTGTCTTTGCGAATGAATAGTCT

DR17006 ATTTCCCAAGACAAAGGCCAAGAATACGGTATATCTGCAAAATGAGGTTTCT  
 DR13006 ATCTCCCAAGACAAAGGCCAAGAACACGCTGTATCTGCAAAATGCGGAACT  
 DR02006 ATCTCCCAAGACAAATTCAGGACACAGTGTATCTGCAAAATGACAGCT

DR01006 GAAACCTGAGGACACGGCGATGTATTACTGTAAAAC-A---GCCCTAC--  
 DR27006 GAAACCTGAGGACACGGCGATGTATTACTGTAAAAT-A---GA--TTC--  
 DR03006 AACCCCTGAAGACACGGCTACGTATTACTGTGCGGCGG---TCCCAGCCC  
 DR11006 GCAACCTGAGGATACGGCCACCTATTACTGCGCGGCAA---GACTGACGG  
 DR24006 GCAACCTGAGGATACGGCCACCTATTACTGCGCGGCAA---GACTGACGG  
 DR16006 GAAACCTGAGGACACGGCCATCTACTTCTGTGCAGCAG---G-----CTC  
 DR19006 GACACCTGAGGACACGGCCATCTACAGTTGTGCGGCAA---C-----CAG  
 DR07006 GAAACCTGAAGACACGGGCACCTATTACTGTGCTG-CA---GAACTAAGT  
 DR16006 GAAACCTGAGGACACGGCCATCTATTACTGCGCGG-CG---GATAGTCCA  
 DR20006 GAAACCTGAGGACACGGCCATGTACTACTGTGCAATCA---CTGAAATTG  
 DR25006 GAAACCTGAGGACACGGCCATGTATTACTGCGCGGTAGATGGTTGGACCC  
 DR20006 CAAACCTGAGGACACGGCCATGTATTACTGTGCG-----CC  
 DR21006 GAACCCGGAGGACACTGCCGACTACTACTGCGCTGCAAATCAATTAGC--  
 DR09006 GAGGCCTGAGGACACGGCCGTGTATTACTGTGCGGCAGATTG-----  
 DR17006 GAAACCTGAGGACACGGCCATCTATTACTGTGCGGCAG-----CGGACCC  
 DR13006 GCAACCTGACGACACTGGCGTGTACTACTGTGCGGCC-----CAA  
 DR02006 GAAACCCGAGGACACGGCCGTGTATTACTGTGGGGCAGT-----

DR01006 -----A-AC--CTGGGGGTTATTGTGGGTA-  
 DR27006 -----GTAC--CCGTGCCATCTCCTTGATG-  
 DR03006 ACTTGGGACCT-----GGCG-CCATT-----CTTGATTGT  
 DR11006 AGATGGGGGCTTGTGATGCGAGATGGGCGACCTTAGC--GACAAGGAC-G  
 DR24006 AGATGGGGGCTTGTGATGCGAGATGGGCGACCTTAGC--GACAAGGAC-G  
 DR16006 GCGTTTTT-CTAGTCCTGTGTTGGGAGCACTTC-TAGAC--TCGAAAGTAG  
 DR19006 TAGTTTTTACTGGTACT-----GCAC-----C---ACG-----G  
 DR07006 GGTGGTAGTTGTGAATTGC---CTTTGC-----TATTTGACTA-----  
 DR16006 TGTTACATGCCGACTATGC---CCGCTCCCCGATACGAGACAGTTTTGG  
 DR20006 AGTGGTATGGGTGCAATTT---AAGGACTACTTTTACT---C-----G  
 DR25006 GGAAGGAAG--GGGGAATCGGGTTAC---CCTGGTCGGTCCAATGTGAA  
 DR20006 GGTTGAA-----TATC---CTATTGCAGAC--ATGTGTT  
 DR21006 ---TGGTGGCTGGTATT-----TGGACCCGAATTACTGG-CTCTCTGTG  
 DR09006 ---GAAATACTGGA---CTTGTGGTGC--CCAGA-CTGG-----AG  
 DR17006 AAGTATATATTATAGTATC-----CTCCNNAT-----  
 DR13006 AAGAAGGATCGTA-----CTAGATGGGC-----CGAGCCT-----  
 DR02006 -----CTCCCTAA--TGGACCGAATTTCT

DR01006 --TGGGTANTGCCTCTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR27006 --T-----CTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR03006 AAAAAGTATAAGTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR11006 TTTGCGTATAACTACTGGGGCCGGGGGACCCAGGTCACCGTCTCCTCACT  
 DR24006 TTTGCGTATAACTACTGGGGCCGGGGGACCCAGGTCACCGTCTCCTCACT  
 DR16006 CGA-CT-ATAACTATTGGGGCCAGGGGATCCAGGTCACCGTCACTCACT  
 DR19006 CGC-CTTATAACGTCTGGGGTCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR07006 CTGGG-----GCCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR16006 CTGGGATGATTTT-----GGCCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR20006 CTGGG-----GCCAGGGGACCCAGGTCACCGTCTCCTCACT  
 DR25006 GATGGTTATAACTATTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAC-  
 DR20006 CGAGAT---ACG---GCGACCCGGGGACCCAGGTCACCGTCTCCTCAC-  
 DR21006 GGTGCATATGCCATCTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCAC-  
 DR09006 GATACTTCGGACAG-TGGGGTCAGGGGGCCAGGTCACCGTCTCCTCACT  
 DR17006 --TGAGTATAAGTACTGGGGCCAGGGGACCCAGGTCACCGTCTCCTCA--

FIGURE 7(3)

DR13006 CGAGAATGGAAACAACCTGGGGGCCAGGGGACCCAGGTCACCGTCTCTCTCA--  
 DR02006 CCAACATGGG--TSCCGGGGGCCAGGGACCCAGGTCACCGTCTCTCT----

DR01006 AG----TTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR27006 AG----TTACCCGTACGAGCTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR03006 AGCTAGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR11006 AG----TTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR24006 AGCTAGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR16006 ----AGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR19006 ----AGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR07006 ----AGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR16006 ----AGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR20006 ----AGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR25006 ---TAGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR20006 ---TAGTTACCCGTACGACGAACCGGACTACGGTTCCTTAATAGAATTC  
 DR11006 ---TAGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR09006 AGCTAGTTACCCGTACGACGTTCCGGACTACGGTTCCTTAATAGAATTC  
 DR17006 -----  
 DR13006 -----  
 DR02006 -----TA

FIGURE 7(4)

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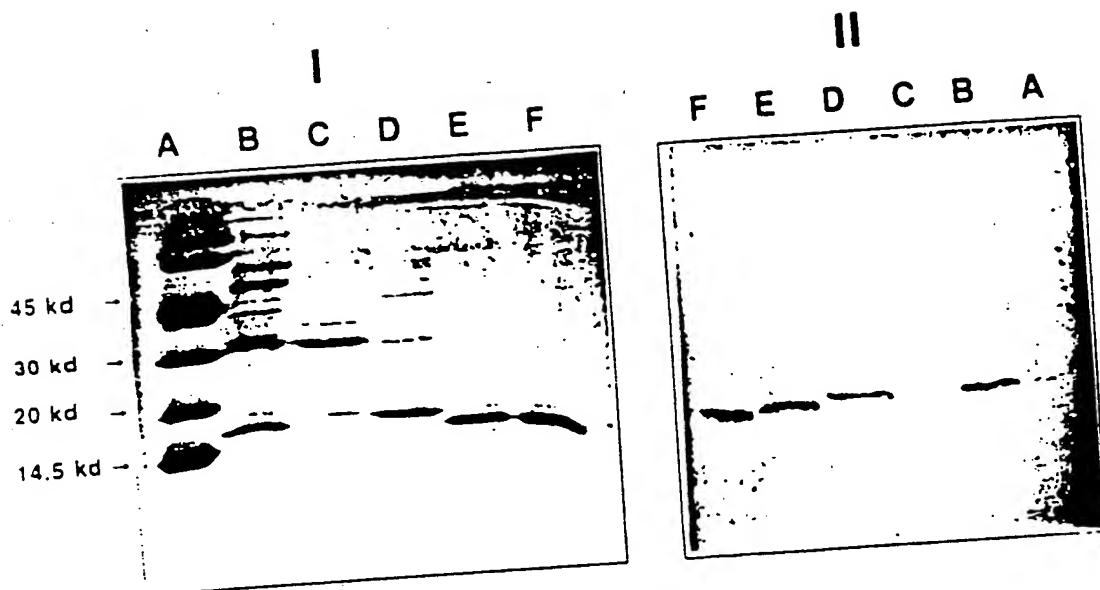


FIGURE 8

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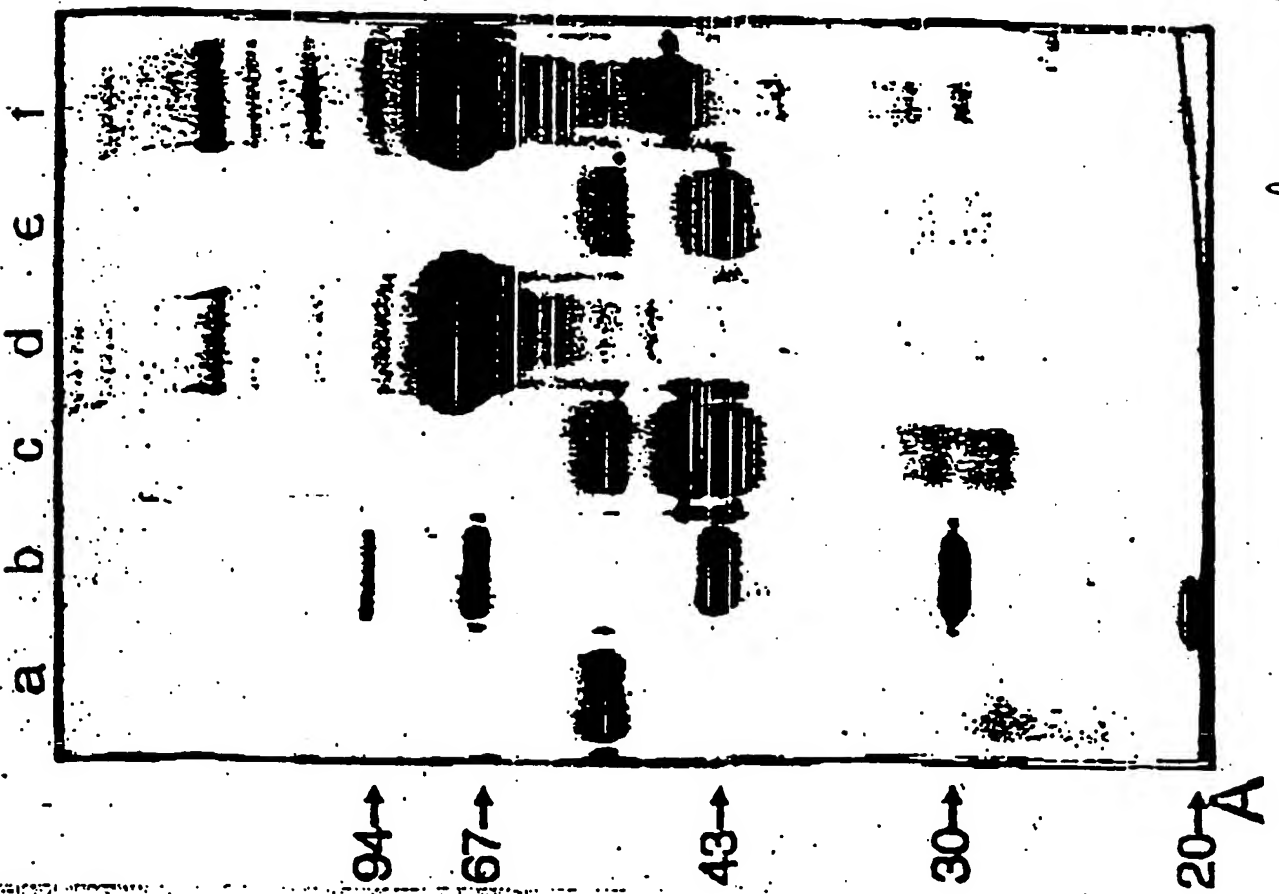
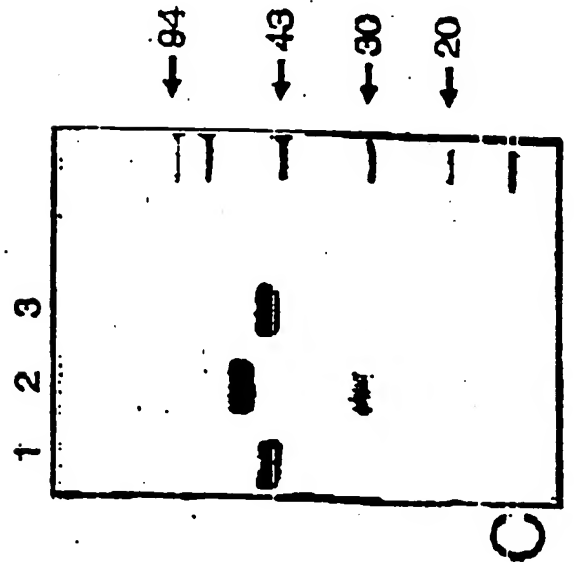
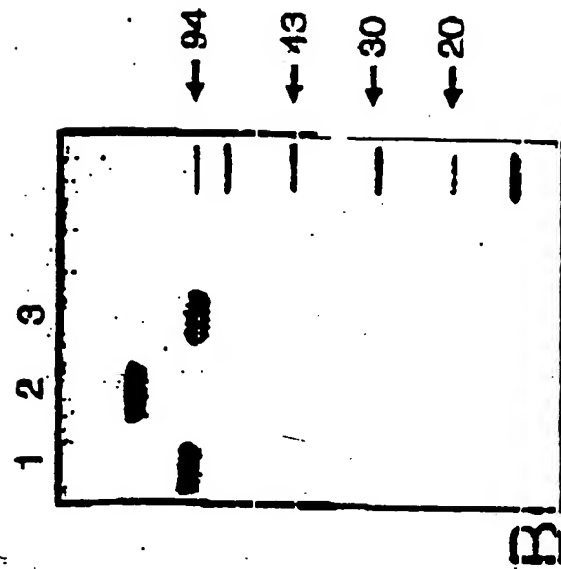
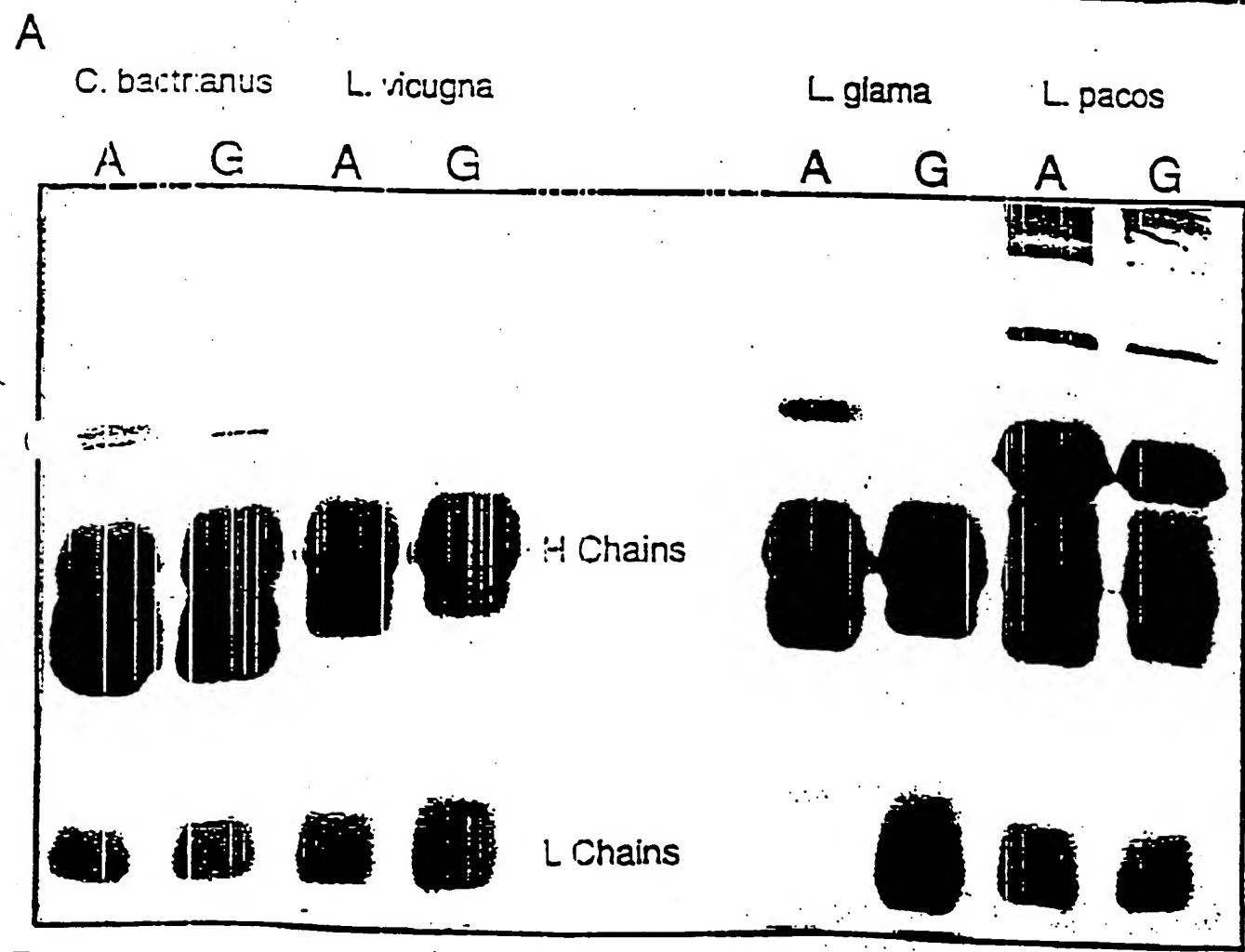
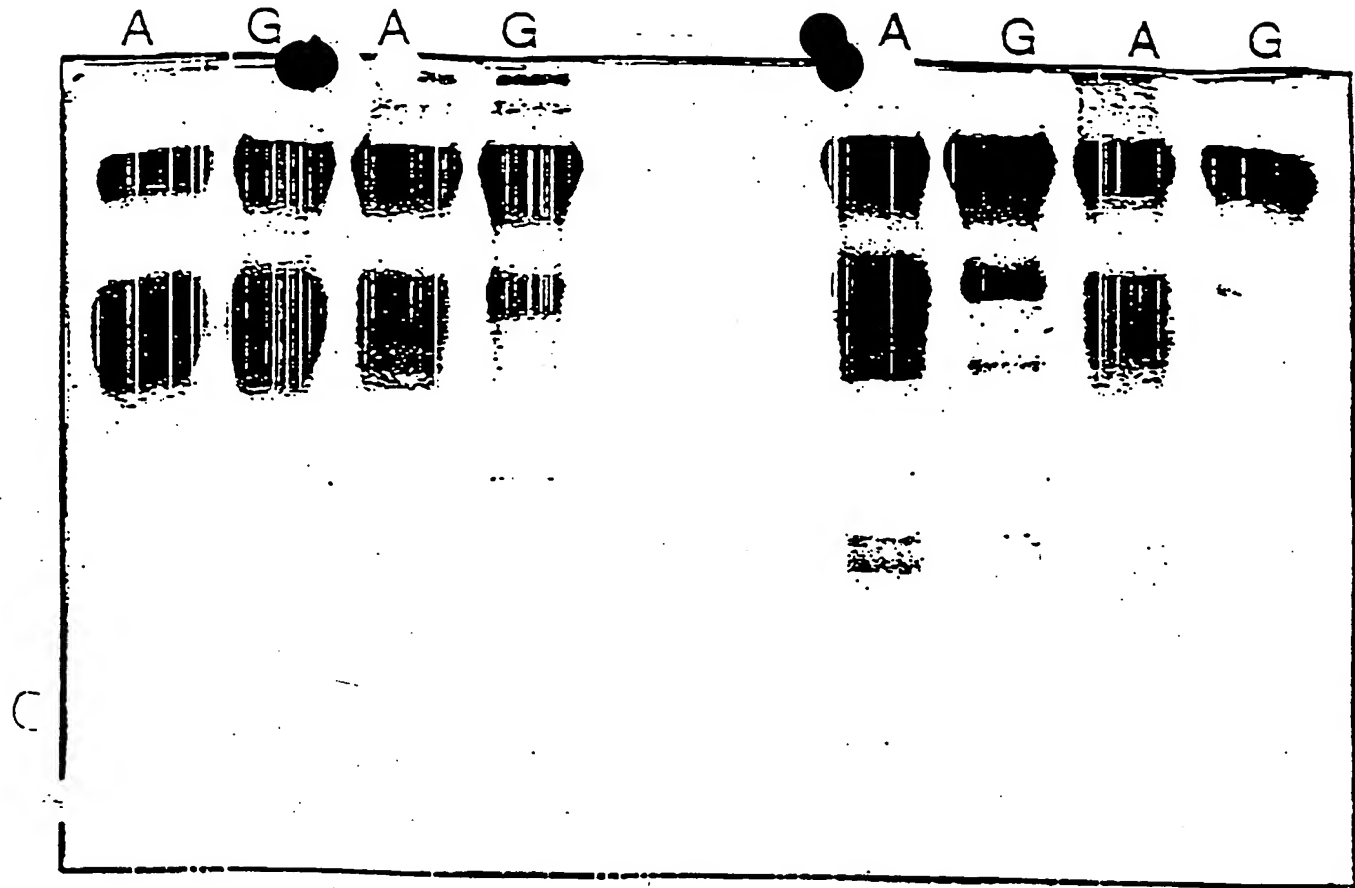
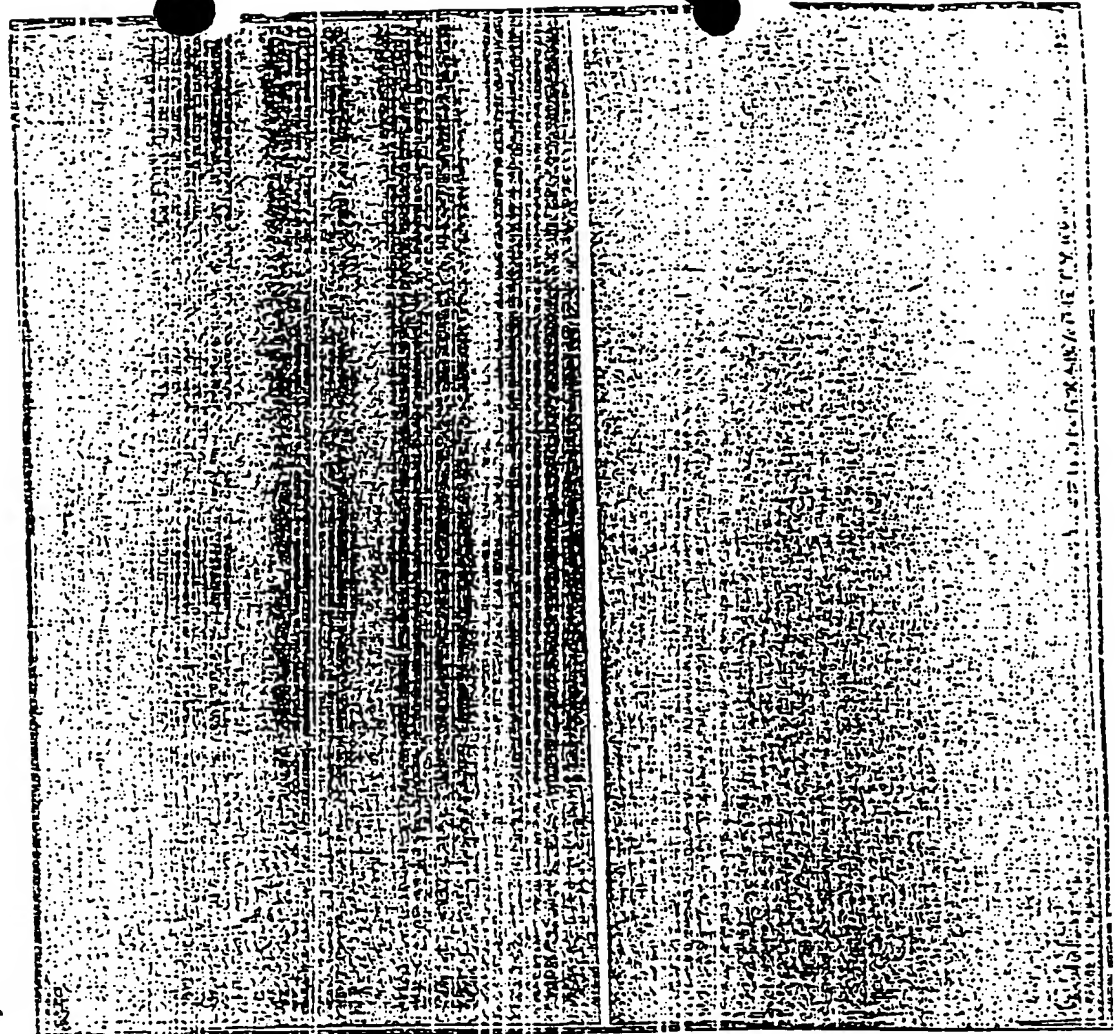


figure 1





A



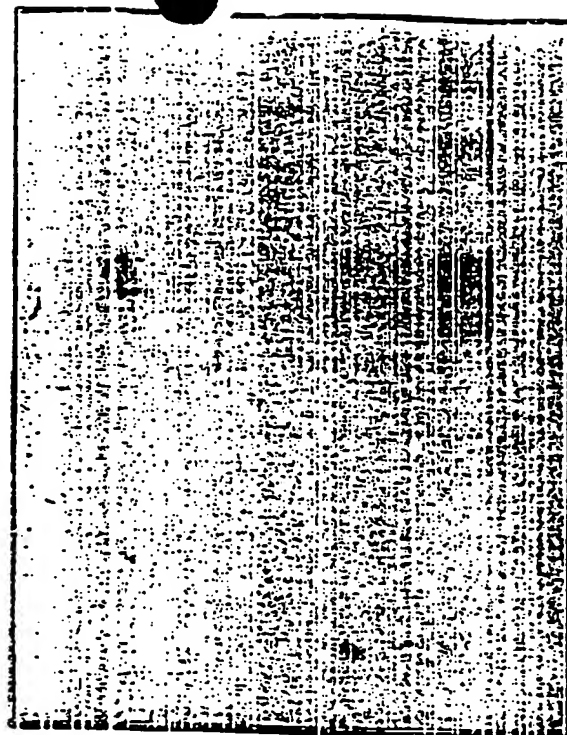
Prot. A	Ig1	Ig2	Ig3	Tot.Ser	Ig1	Ig2	Ig3	Tot.Ser
Control		T. evansi infected				Healthy		
Counts: 5ul 65	1258	1214	2700	2978	147	157	160	107

figure 3 (1)

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3

B



Ig1 Ig2 Ig3

Ig1 Ig2 Ig3

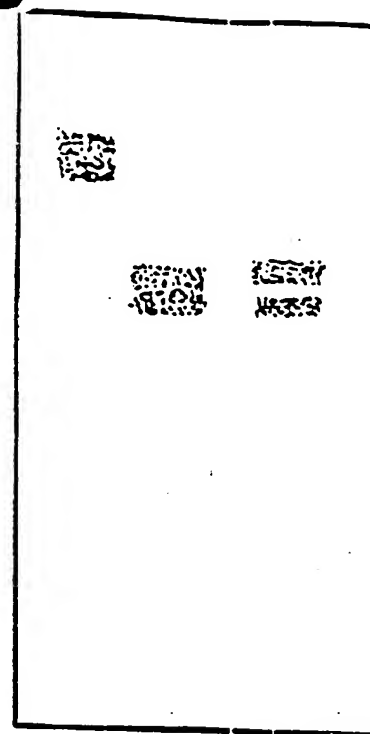
-healthy

T. evansi infected

← 94

← 67

← 43



Ig1

Ig2

Ig3

Ponceau Red

figure 3 (2)

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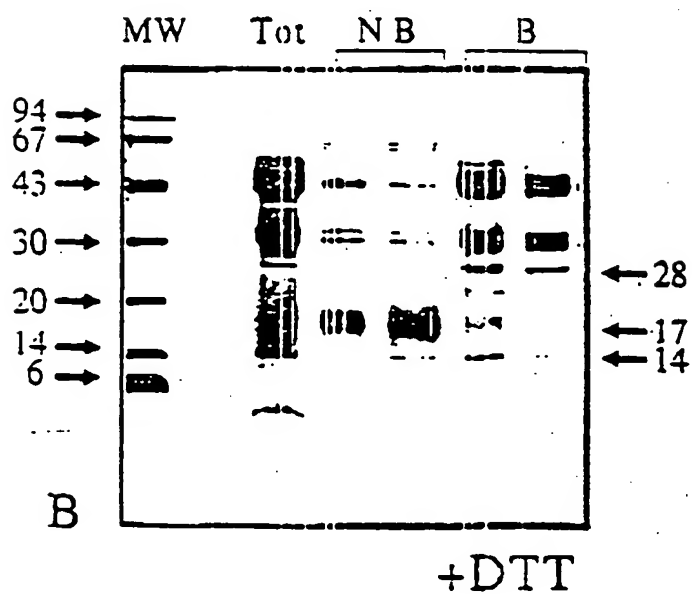
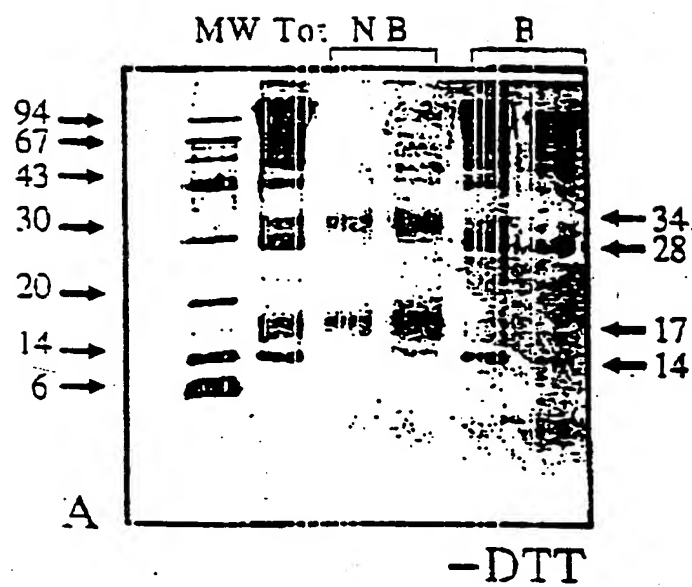


Fig 4 Analysis of IgG<sub>3</sub> Papain Fragments by SDS - PAGE